

Table S4. The predicted virulence factors in strains WUSP070 and WUSP074

Gene ID	Start	End	Length	Strand	Annotation
WUSP070					
M0P24_RS00375	69330	70343	1014	+	dTDP-glucose 4,6-dehydratase
M0P24_RS03135	604385	605693	1299	+	PssD/Cps14F family polysaccharide biosynthesis glycosyltransferase dTDP-4-
M0P24_RS03425	675712	676566	855	+	dehydrorhamnose 3,5-epimerase family protein
M0P24_RS03440	678853	679659	807	+	phosphopyruvate hydratase
M0P24_RS03445	679659	680870	1212	+	glucose-1-phosphate thymidyltransferase RfbA
M0P24_RS05770	1142023	1142520	498	-	glycosyltransferase dTDP-4-
M0P24_RS05775	1142532	1143008	477	-	dehydrorhamnose reductase
M0P24_RS05815	1149837	1150745	909	+	trigger factor
M0P24_RS06415	1268062	1269111	1050	-	ABC transporter permease
M0P24_RS06420	1269286	1269879	594	-	UTP--glucose-1-phosphate uridyltransferase GalU
M0P24_RS06425	1269879	1270748	870	-	type I glyceraldehyde-3-phosphate dehydrogenase
M0P24_RS09160	1805305	1806588	1284	-	ABC transporter ATP-binding protein
M0P24_RS10995	2140907	2141821	915	+	LysR family transcriptional regulator
WUSP074					
M0P28_RS01700	294896	296179	1284	+	dTDP-glucose 4,6-dehydratase
M0P28_RS04060	768445	769314	870	+	GbpC/Spa domain-containing protein
M0P28_RS04065	769314	769907	594	+	dTDP-4-dehydrorhamnose 3,5-

Gene ID	Start	End	Length	Strand	Annotation
M0P28_RS04070	770082	771131	1050	+	epimerase family protein phosphopyruvate hydratase
M0P28_RS04195	799732	801387	1656	-	glucose-1-phosphate thymidyltransferase RfbA
M0P28_RS04645	890694	891602	909	-	dTDP-4- dehydrorhamnose reductase
M0P28_RS07390	1443721	1444527	807	-	trigger factor
M0P28_RS07405	1446814	1447668	855	-	ABC transporter permease
M0P28_RS07950	1555210	1560105	4896	-	UTP--glucose-1- phosphate uridylyltransferase GalU
M0P28_RS08135	1596129	1597427	1299	-	type I glyceraldehyde- 3-phosphate dehydrogenase
M0P28_RS10980	2165137	2166150	1014	-	LysR family transcriptional regulator
M0P28_RS11380	2233620	2234534	915	+	NFACT RNA binding domain-containing protein